

Figure 1: 121P1F1 SSH sequence of 254 nucleotides (SEQ ID: )

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1 GATCACAGTC TTTGTATTTT TCTACTTCTG CCTTTAGCTG TTCCCTTTGG TCTCGAAGTG
61 AAGAAAGCTC TTTTGCTAGC CTGGTTCGCT CTTCCGTTTC ACATCGGCCA ATTTTAGCTT
121 TCTCAATGCT TTTCTGTAGG CTTGCATGCT TTTGACTTCC CTCAGACAAC TGAGATTCCA
181 GAACCTCCAA CTTATGTTTC CTTGCATGAA GAGCTTTACT TGGAAAAGCC CAATAATAAT
241 TAGAAGTTCC GATC

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Figure 2: The cDNA and Amino Acid Sequence(s)

Figure 2A. The cDNA (SEQ ID. NO. : ) and amino acid sequence (SEQ ID. NO. : ) of 121P1F1. The start methionine is underlined. The open reading frame extends from nucleic acid 82-699 including the stop codon.

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1 ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcgggcccgccagc
1 M S K K K G L S A E E K R
61 ggaagccccctgcgcccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCTAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAAGTCTTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I R Q A N K V A K E A A N R W T D N I
541 GAAATACGCCAAGCAAATAAAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATA
174 F A I K S W A K R K F G F E E N K I D R
601 TTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGA
194 T F G I P E D F D Y I D *
661 ACTTTTGGAAATCCAGAAGACTTTTGACTACATAGACTAAAtattccatgggtggtgaagg
721 atgtacaagcttgtgaatatgtaaattttaactattatctaactaagtgtactgaattg
781 tcgtttgcctgtaaactgtgttttatcatttttattaatgttaaataaagtgtaaaatgcaaa
841 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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Figure 2B. The cDNA (SEQ ID. NO. :       ) and amino acid sequence (SEQ ID. NO. :       ) of 121P1F1 splice variant 1A. The start methionine is underlined. The open reading frame extends from nucleic acid 82-462 including the stop codon.

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1 ccaaaatcaaacgcgtccgggctgtcccgccccctctccccaagcgcgggcccgccagc
1      M S K K K G L S A E E K R
61 ggaagccctgcgcccgcgcATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q D
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGGAC
94 P G C C F H E I I K V S Y Y R K F W L G
361 CCTGGCTGCTGCTTCCATGAAATAATTAAAGTCTCCTATTATAGAAAATTCTGGCTGGGC
114 A V A H A C N P S T L G G *
421 GCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAggcgggcagatcacgagg
481 tgactttccccccacccccacatgaagtgcaagatggagtgtgtctgaggggaagtcaaaagc
541 atgcaagcctacagaaaagcattgagaaagctaaaattggccgatgtgaaacggaagagc
601 gaaccaggctagcaaaagagctttcttcacttcgagaccaaagggaacagctaaaggcag
661 aagtagaaaaatacaaaagactgtgatccgcaagttgtggaagaaatacgccaagcaaata
721 aagtagccaaagaagctgctaacagatggactgataacatattcgcaataaaatcttggg
781 ccaaaagaaaatttgggtttgaagaaaataaaattgatagaacttttgggaattccagaag
841 acttttgactacatagactaaaatattccatgggtggtgaaggatgtacaagcttgtgaata
901 tgtaaatttttaactattatctaactaagtgtactgaattgtcgtttgctgttaactgtg
961 tttatcattttattaatgttaataaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaa

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Figure 2C. The cDNA (SEQ ID. NO. :\_\_\_\_) and amino acid sequence (SEQ ID. NO. :\_\_\_\_) of 121P1F1 splice variant 1B. The start methionine is underlined. The open reading frame extends from nucleic acid 501-860 including the stop codon.

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1  ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcgggcccgccagc
61  ggaagccccctgcgcccgcgccatgtcaaagaaaaaggactgagtgcagaagaaaagaga
121 actcgcatgatggaaatattttctgaaacaaaagatgtattttcaattaaaagacttggag
181 aagattgctcccaaagagaaaggcattactgctatgtcagtaaaagaagtccttcaaagc
241 ttagttgatgatggatggttggtgactgtgagaggatcggaacttctaattattattgggct
301 ttccaagtaaaagctcttcatgcaaggaaacataagttggagggttctggaatctcaggac
361 cctggctgctgcttccatgaaataattaaagtctcctattatagaaaattctggctgggc
421 gcagtggctcacgcctgtaatcccagcactttgggagggtgaggcgggcagatcacgagg
1      M K C K M E L S E G S Q K H
481 tgactttccccccacccccacATGAAGTGAAGATGGAGTTGTCTGAGGGAAGTCAAAAGC
15   A S L Q K S I E K A K I G R C E T E E R
541 ATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGC
35   T R L A K E L S S L R D Q R E Q L K A E
601 GAACCAGGCTAGCAAAAGAGCTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAG
55   V E K Y K D C D P Q V V E E I R Q A N K
661 AAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATA
75   V A K E A A N R W T D N I F A I K S W A
721 AAGTAGCCAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGG
95   K R K F G F E E N K I D R T F G I P E D
781 CCAAAAGAAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGAATTCCAGAAG
115  F D Y I D *
841 ACTTTGACTACATAGACTAAaatattccatgggtgggtgaaggatgtacaagcttgtgaata
901 tgtaaattttaaaactattatctaactaagtgtactgaattgtcgtttgctgtaaactgtg
961 tttatcattttattaatgttaataaaagtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaa
1021 aaaaaaaa

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Figure 2D. The cDNA (SEQ ID. NO. :\_\_\_\_) and amino acid sequence (SEQ ID. NO. :\_\_\_\_) of 121P1F1 splice variant 2. The start methionine is underlined. The open reading frame extends from nucleic acid 82-450 including the stop codon.

```

1 ccaaaatcaaacgcgtccgggctgcccgcctctccccaagcgcgggcccggccagc
1      M S K K K G L S A E E K R
61 ggaagccccctgcgccccgcgccATGTCAAAGAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTTAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T A K Q I K *
421 CGATGTGAAACGGCCAAGCAAATAAAGTAGccaaagaagctgctaacagatggactgata
481 acatattcgcaataaaaatcttggggccaaaagaaaatttgggtttgaagaaaataaaattg
541 atagaacttttgggaattccagaagactttgactacatagactaaaatattccatgggtggt
601 gaaggatgtacaagcttgtgaatatgtaaattttaaactattatctaactaagtgtactg
661 aattgtcgtttgcctgtaactgtgtttatcattttattaatgttaaataaagtgtaaaat
721 gcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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Figure 2E. The cDNA (SEQ ID. NO. : \_\_\_\_ ) and amino acid sequence (SEQ ID. NO. : \_\_\_\_ ) of  
121P1F1 splice variant 3. The start methionine is underlined. The open reading frame extends from nucleic acid  
82-654 including the stop codon.

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1 ccaaaatcaaacgcgtccgggctgtcccgccctctccccaagcgcgggcccgccagc
1           M S K K K G L S A E E K R
61 ggaagccccctgcgcccgcgccATGTCAAAGAAAAAAGGACTGAGTGCAGAAGAAAAGAGA
14 T R M M E I F S E T K D V F Q L K D L E
121 ACTCGCATGATGGAAATATTTTCTGAAACAAAAGATGTATTTCAATTAAAAGACTTGGAG
34 K I A P K E K G I T A M S V K E V L Q S
181 AAGATTGCTCCCAAAGAGAAAGGCATTACTGCTATGTCAGTAAAAGAAGTCCTTCAAAGC
54 L V D D G M V D C E R I G T S N Y Y W A
241 TTAGTTGATGATGGTATGGTTGACTGTGAGAGGATCGGAACCTTCTAATTATTATTGGGCT
74 F P S K A L H A R K H K L E V L E S Q L
301 TTTCCAAGTAAAGCTCTTCATGCAAGGAAACATAAGTTGGAGGTTCTGGAATCTCAGTTG
94 S E G S Q K H A S L Q K S I E K A K I G
361 TCTGAGGGAAGTCAAAAGCATGCAAGCCTACAGAAAAGCATTGAGAAAGCTAAAATTGGC
114 R C E T E E R T R L A K E L S S L R D Q
421 CGATGTGAAACGGAAGAGCGAACCAGGCTAGCAAAGAGCTTTCTTCACTTCGAGACCAA
134 R E Q L K A E V E K Y K D C D P Q V V E
481 AGGGAACAGCTAAAGGCAGAAGTAGAAAAATACAAAGACTGTGATCCGCAAGTTGTGGAA
154 E I H N I F A I K S W A K R K F G F E E
541 GAAATACATAACATATTCGCAATAAAATCTTGGGCCAAAAGAAAATTTGGGTTTGAAGAA
174 N K I D R T F G I P E D F D Y I D *
601 AATAAAATTGATAGAACTTTTGAATTCCAGAAGACTTTGACTACATAGACTAAaatatt
661 ccatggtggtgaaggatgtacaagcttgtgaatatgtaaattttaactattatctaact
721 aagtgtactgaattgtcgttttgctgtaactgtgtttatcattttattaatgttaaataa
781 agtgtaaaatgcaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

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Figure 2F. The cDNA (SEQ ID. NO. :\_\_\_\_) and amino acid sequence (SEQ ID. NO. :\_\_\_\_) of  
121P1F1 splice variant 4. The start methionine is underlined. The open reading frame extends from nucleic acid  
281-853 including the stop codon.

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1  gttttctgtattgtaatatgtagagcacattccagaactgctcagtttcgagttacctaa
61  tggatcttcactgtgtgcccaattagtcgattttctgtgaaaacgccccggtttctgccaaa
121 gggcaggagtcgctgctcttgtgccgggtgctgctggttgtgtagggcgctgttgctttt
181 ttaaggacgctctgcactgaattaggcttcctcgtgggtcatgatcagttaagtcctgtc
1                                     M M E I F S E
241 aaagaaaaaaggactgagtgcagaagaaaagagaactcgcATGATGGAAATATTTTCTGA
8  T K D V F Q L K D L E K I A P K E K G I
301 AACAAAAGATGTATTTCAATTAAAGACTTGGAGAAGATTGCTCCCAAAGAGAAAGGCAT
28  T A M S V K E V L Q S L V D D G M V D C
361 TACTGCTATGTCAGTAAAGAAGTCCTTCAAAGCTTAGTTGATGATGGTATGGTTGACTG
48  E R I G T S N Y Y W A F P S K A L H A R
421 TGAGAGGATCGGAACTTCTAATTATTATTGGGCTTTTCCAAGTAAAGCTCTTCATGCAAG
68  K H K L E V L E S Q L S E G S Q K H A S
481 GAAACATAAGTTGGAGGTTCTGGAATCTCAGTTGTCTGAGGGAAGTCAAAGCATGCAAG
88  L Q K S I E K A K I G R C E T E E R T R
541 CCTACAGAAAAGCATTGAGAAAGCTAAAATTGGCCGATGTGAAACGGAAGAGCGAACCAG
108 L A K E L S S L R D Q R E Q L K A E V E
601 GCTAGCAAAGAGCTTTTCTTCACTTCGAGACCAAAGGGAACAGCTAAAGGCAGAAGTAGA
128 K Y K D C D P Q V V E E I R Q A N K V A
661 AAAATACAAAGACTGTGATCCGCAAGTTGTGGAAGAAATACGCCAAGCAAATAAAGTAGC
148 K E A A N R W T D N I F A I K S W A K R
721 CAAAGAAGCTGCTAACAGATGGACTGATAACATATTCGCAATAAAATCTTGGGCCAAAAG
168 K F G F E E N K I D R T F G I P E D F D
781 AAAATTTGGGTTTGAAGAAAATAAAATTGATAGAACTTTTGGAAATCCAGAAGACTTTGA
188 Y I D *
841 CTACATAGACTAAaatattccatgggtggtgaaggatgtacaagcttgtgaatatgtaa
901 tttaaactattatctaactaagtgtactgaattgtcgtttgctgtactgtgtttatca
961 ttttattaatgttaaataaagtgtaaaatgcagatgttcttcaccccttttggtagaaca
1021 aaagcaggatgataaccatatccccccagtgtcatcaaagtaggacactaaaaatccat
1081 ccatctcagtcaaagtcgagcgccgcgaatttagtagtagtagcgccgctctagagga
1141 tccaagcttacgtacgcgtgcatgcgacgtcatagctcttctatagtgtcacctaaattc
1201 aagtt

```

**Figure 3:**

**Figure 3A. Amino acid sequence of 121P1F1 (SEQ ID. NO. : \_\_\_\_).** The 121P1F1 protein has 205 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV  
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER  
121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIRQANK VAKEAANRWT DNIFAIKSWA  
181 KRKFGFEENK IDRTFGIPED FDYID

**Figure 3B. Amino acid sequence of 121P1F1 splice variant 1A (SEQ ID. NO. : \_\_\_\_).** The 121P1F1 splice variant 1A protein has 126 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV  
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQDPGCCFHE IIKVSYYRKF WLGAVAHACN  
121 PSTLGG

**Figure 3C. Amino acid sequence of 121P1F1 splice variant 1B (SEQ ID. NO. : \_\_\_\_).** The 121P1F1 splice variant 1B protein has 119 amino acids.

1 MKCKMELSEG SQKHASLQKS IEKAKIGRCE TEERTRLAKE LSSLRDQREQ LKAEVEKYKD  
61 CDPQVVEEIR QANKVAKEAA NRWTDNIFAI KSWAKRKFGF EENKIDRTFG IPEDFDYID

**Figure 3D. Amino acid sequence of 121P1F1 splice variant 2 (SEQ ID. NO. : \_\_\_\_).** The 121P1F1 splice variant 2 protein has 122 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV  
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETAKQ  
121 IK

Figure 3E. Amino acid sequence of 121P1F1 splice variant 3 (SEQ ID. NO. : \_\_\_\_). The 121P1F1 splice variant 3 protein has 190 amino acids.

1 MSKKKGLSAE EKRTRMMEIF SETKDVFQLK DLEKIAPKEK GITAMSVKEV LQSLVDDGMV  
61 DCERIGTSNY YWAFPSKALH ARKHKLEVLE SQLSEGSQKH ASLQKSIEKA KIGRCETEER  
121 TRLAKELSSL RDQREQLKAE VEKYKDCDPQ VVEEIHNIFA IKSWAKRKFG FEENKIDRTF  
181 GIPEDFDYID

Figure 3F. Amino acid sequence of 121P1F1 splice variant 4 (SEQ ID. NO. : \_\_\_\_). The 121P1F1 splice variant 4 protein has 190 amino acids.

1 MMEIFSETKD VFQLKDLEKI APKEKGITAM SVKEVLQSLV DDGMVDCERI GTSNYYWAFP  
61 SKALHARKHK LEVLESQLE GSQKHASLQK SIEKAKIGRC ETEERTRLAK ELSSLRDQRE  
121 QLKAEVEKYK DCDPQVVEEI RQANKVAKEA ANRWTDNIFA IKSWAKRKFG FEENKIDRTF  
181 GIPEDFDYID

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Figure 4A

Amino Acid Alignments.

Alignment of 121P1F1 protein and its variants.

A) CLUSTAL W alignment of 121P1F1 and variants 1-3.

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121P1F01      -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLKLEKIAPKEKGITAMSVKE
sv1A          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLKLEKIAPKEKGITAMSVKE
sv1B          -----MKCKMELSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
sv-2          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLKLEKIAPKEKGITAMSVKE
sv-3          -----MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLKLEKIAPKEKGITAMSVKE

121P1F01      VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQK-HASLQKS-I
sv1A          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQDP-GCCF-HEIIKVSYY
sv1B          QLKAEEVEK-YKDCDPQVVEEIRQANKVAKAANRWTDNIFAISWAKRKFGEENKID--
sv-2          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQK-HASLQKS-I
sv-3          VLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQK-HASLQKS-I

121P1F01      EKAKIGRCETEERTRLAKELSSLRDQREQLKAEEVEKYKDCDPQVVEEIRQANKVAKAAN
sv1A          RKFVLGAVAHACNPSTLGG-----
sv1B          RTFGIPEDFDYID-----
sv-2          EKAKIGRCETAKQIK-----
sv-3          EKAKIGRCETEERTRLAKELSSLRDQREQLKAEEVEKYKDCDPQVVEEIHNIFAISWAKR

121P1F01      RWTDNIFAISWAKRKFGEENKIDRTFGIPEDFDYID
sv1A          -----
sv1B          -----
sv-2          -----
sv-3          KFGFEENKIDRTFGIPEDFDYID-----

```

Figure 4B

Clustal alignment of 121P1F1 and variants 1A and 4

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      1      15 16      30 31      45 46      60 61      75 76      90
1 121P1F01 MSKKKGLSAEEKRTR MMEIFSETKDVFLQK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCERIGTSNYYWAF SKALHARKHKLEVLE
2 sv-4      ----- MMEIFSETKDVFLQK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCERIGTSNYYWAF SKALHARKHKLEVLE
3 sv-1A     MSKKKGLSAEEKRTR MMEIFSETKDVFLQK DLEKIAPKEKGITAM SVKEVLQSLVDDGMV DCERIGTSNYYWAF SKALHARKHKLEVLE

      91      105 106      120 121      135 136      150 151      165 166      180
1 121P1F01 SQLSEGSQKHASLQK SIEKAKIGRCETEER TRLAKELSSLRDQRE QLKAEEVEKYKDCDPQ VVEEIRQANKVAKA ANRWTDNIFAISWA
2 sv-4      SQLSEGSQKHASLQK SIEKAKIGRCETEER TRLAKELSSLRDQRE QLKAEEVEKYKDCDPQ VVEEIRQANKVAKA ANRWTDNIFAISWA
3 sv-1A     SQDPGCCPFHEIIKVS YYRKFWLG----- -----AVAHACNP STLGG-----

      181      195 196      210 211
1 121P1F01 KRKFGFEENKIDRTF GIPEDFDYID 205
2 sv-4      KRKFGFEENKIDRTF GIPEDFDYID 190
3 sv-1A     ----- 126

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# Figure 4C

## C) Alignment with human GAJ

Identities = 205/205 (100%), Positives = 205/205 (100%)

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121P1: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER 120
          DCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER
Sbjct: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQLESGSQKHASLQKSIEKAKIGRCETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA 180
          TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA
Sbjct: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWDNIFAISWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEENKIDRTFGIPEDFDYID
Sbjct: 181  KRKFGFEENKIDRTFGIPEDFDYID 205

```

## Figure 4D

### D) Alignment with closest mouse homolog, a hypothetical 24.2 KDa protein.

Identities = 183/205 (89%), Positives = 193/205 (93%)

```
121P1: 1   MSKKKGLSAEEKRTRMMEIFSETKDVFLQKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV 60
          MSKK+GLS EEKTRMMEIF ETKDVFLQKDLEK+APKEKGITAMSVKEVLQSLVDDGMV
Sbjct: 1   MSKKRGLSGEEKRTRMMEIFFETKDVFLQKDLEKLAPKEKGITAMSVKEVLQSLVDDGMV 60

121P1: 61   DCERIGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGRCETEER 120
          DCERIGTSNYYWAFPSKALHARK KLE L SQLSEGSQKHA LQKSIEKA++GR ETEER
Sbjct: 61   DCERIGTSNYYWAFPSKALHARKRKLEALNSQSEGSQKHADLQKSIEKARVGRQETEER 120

121P1: 121  TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180
          LAKEL S RDQR+QLKAEVEKY++CDPQVVEEIR+ANKVAKEAANRWTDNIFAIKSWA
Sbjct: 121  AMLAKELFSFRDQRQQLKAEVEKYRECDPQVVEEIREANKVAKEAANRWTDNIFAIKSWA 180

121P1: 181  KRKFGFEENKIDRTFGIPEDFDYID 205
          KRKFGFEE+KID+ FGIPEDFDYID
Sbjct: 181  KRKFGFEESKIDKNFGIPEDFDYID 205
```

# Figure 4E

E. >gi|1175412|sp|Q09739|YA53\_SCHPO HYPOTHETICAL 24.2 KD PROTEIN C13A11.03  
IN CHROMOSOME I  
gi|7490680|pir||T37610 hypothetical coiled-coil protein - fission yeast  
(Schizosaccharomyces pombe)  
gi|984224|emb|CAA90804.1| (Z54096) hypothetical coiled-coil protein  
[Schizosaccharomyces pombe]  
Length = 210

Score = 121 bits (305), Expect = 5e-27

Identities = 81/202 (40%), Positives = 115/202 (56%), Gaps = 6/202 (2%)

Query: 5 KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64  
KGLS EKR R+ IF ++KD FQLK++EK+ K K I +VK+VLQSLVDD +V E+  
Sbjct: 4 KGLSLAEKRRRLEAIFHDSKDFQLKEVEKLGSK-KQIVLQTVKDVQLQSLVDDNIVKTEK 62

Query: 65 IGTSNYYWAFPSKALHARKHKLEVLESQSEGSQKHASLQKSIEKAKIGR----CETEER 120  
IGTSNYYW+FPS A +R+ L L++QL + QK +L ++I K R E +  
Sbjct: 63 IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTEENDAN 122

Query: 121 TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAISWA 180  
+ L + + + LK ++ C+P+ E + K EAAN WTD I + ++  
Sbjct: 123 QYTLELLHAKESSELKLLKTQLSNLNHCNPETFELKNENTKKYMEANLWTDQIHTLIAFC 182

Query: 181 KRKFGFEENKIDRTFGIPEDFD 202  
R G + N+I IPED D  
Sbjct: 183 -RDMGADTNQIREYCSIPEDLD 203

## Figure 5A

### 121P1F1 Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

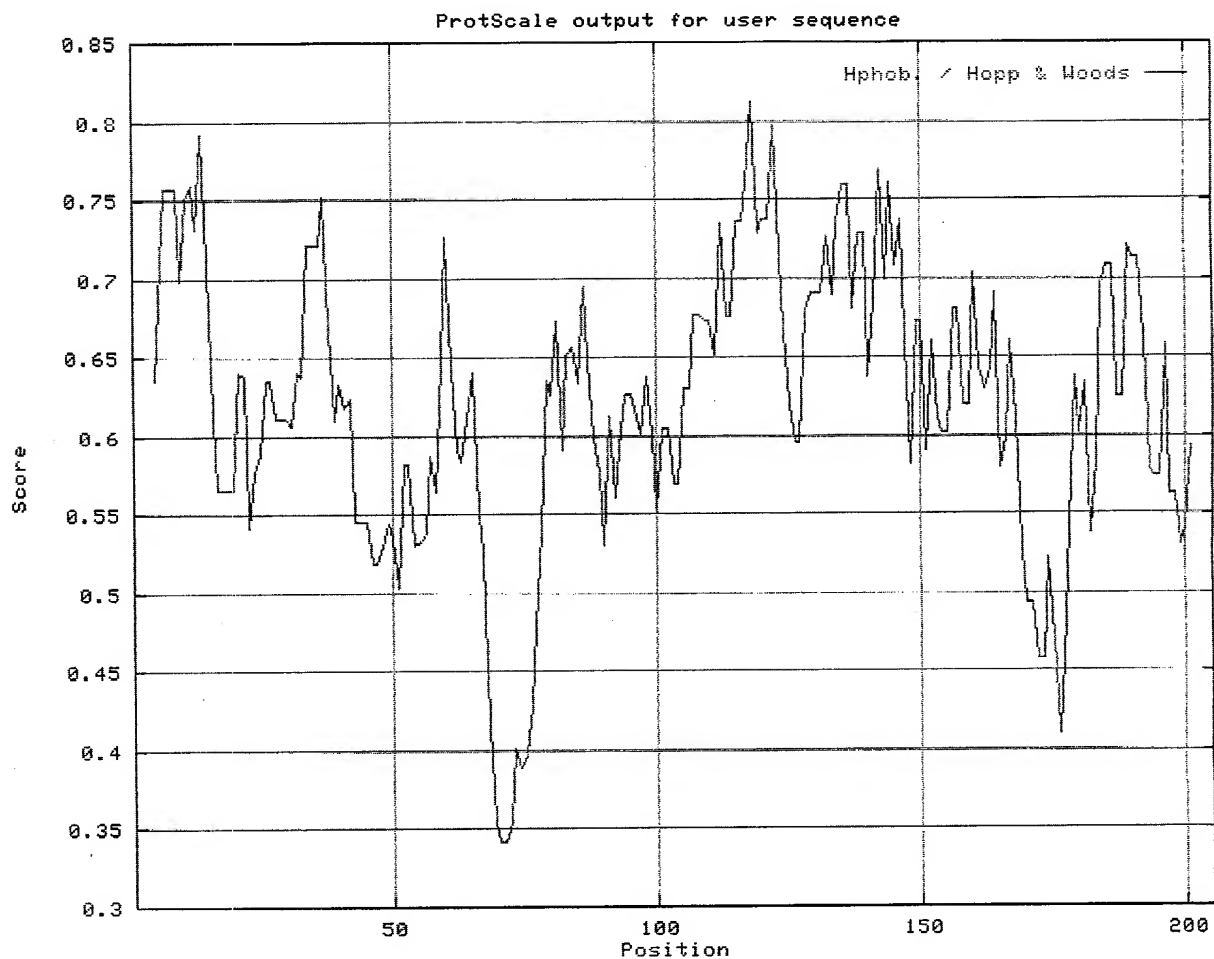


Figure 5B

121P1F1 variant 1a Hydrophilicity profile

(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

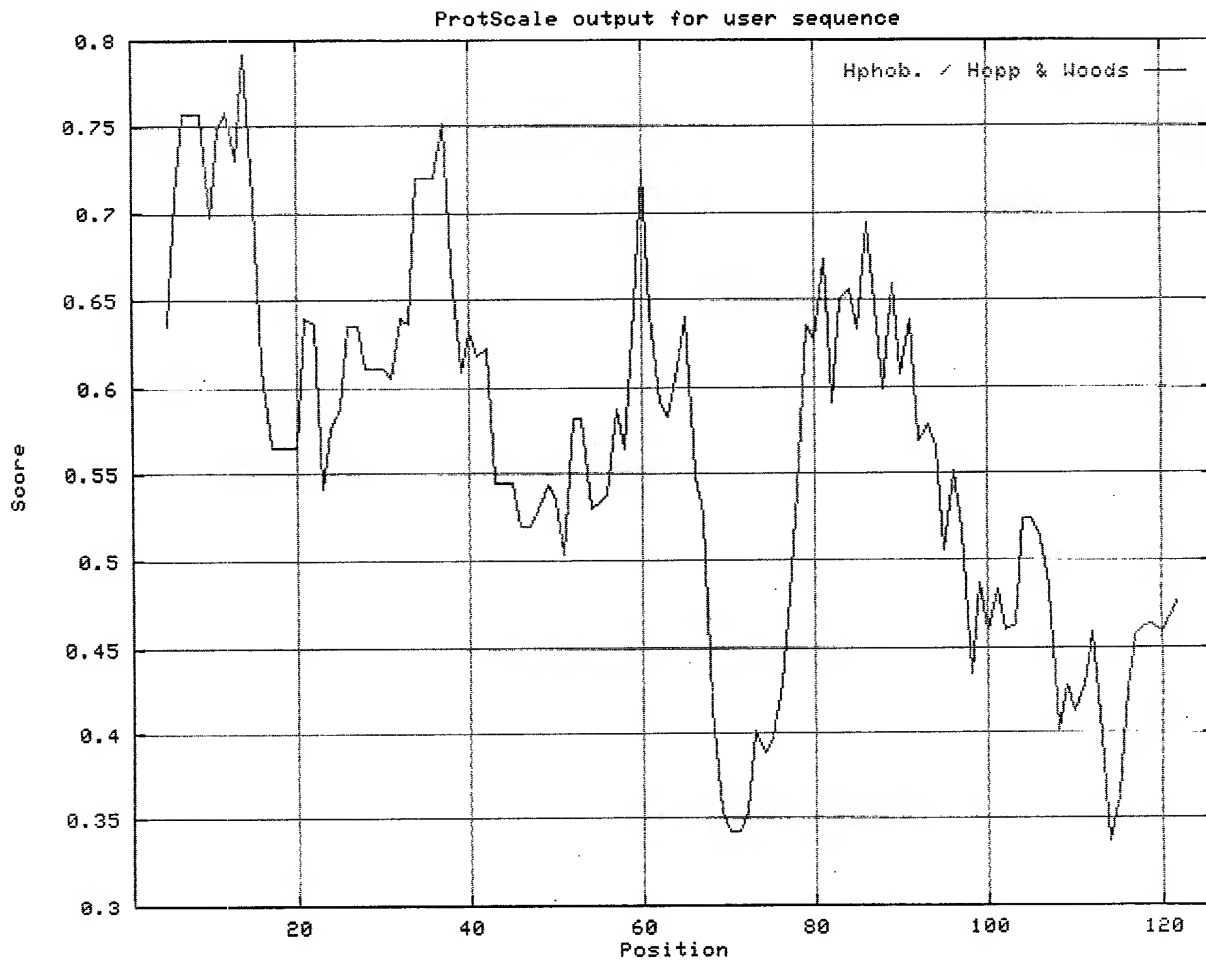


Figure 6A  
121P1F1 Hydropathicity Profile  
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

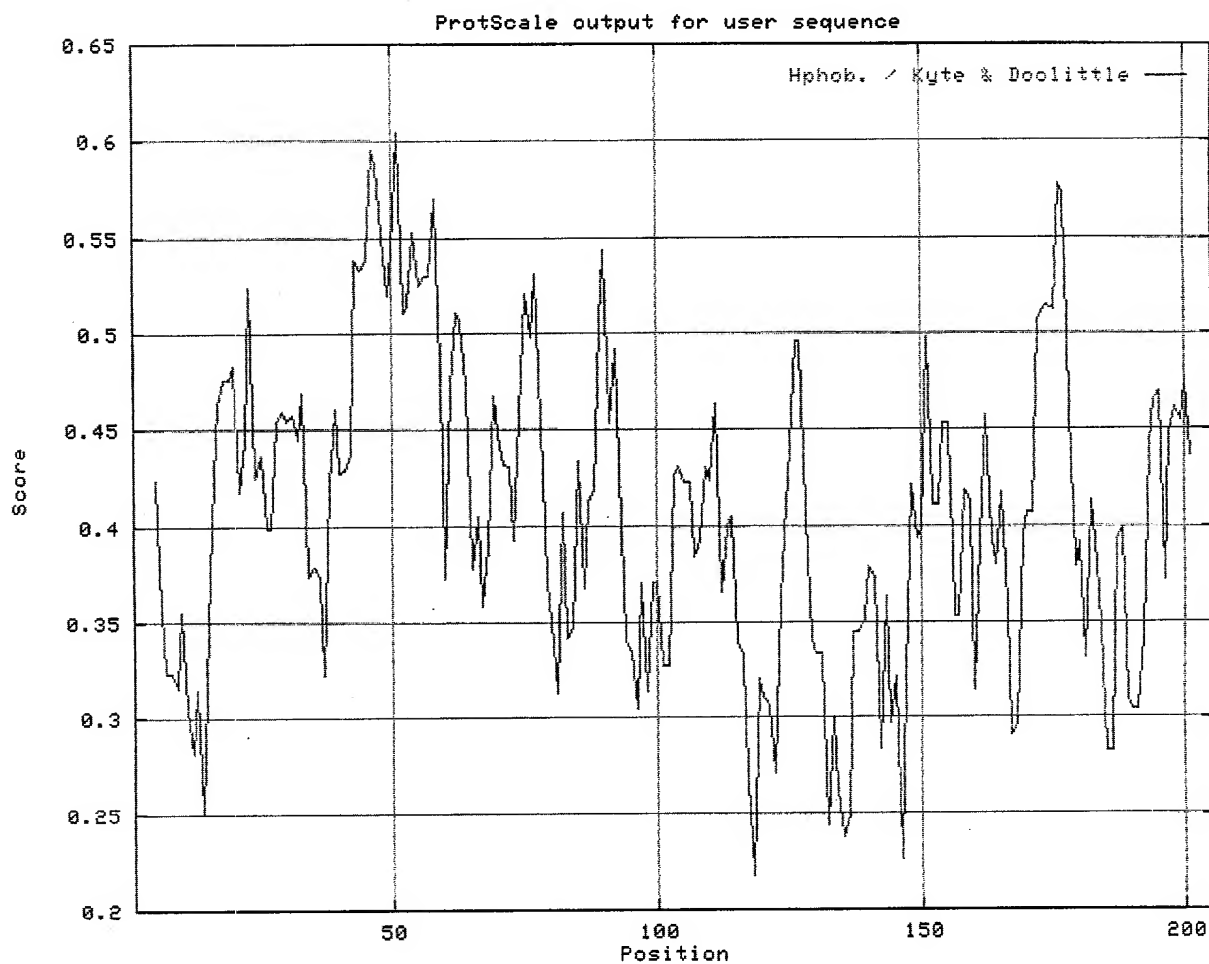


Figure 6B  
 121P1F1 variant 1a Hydropathicity Profile  
 (Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

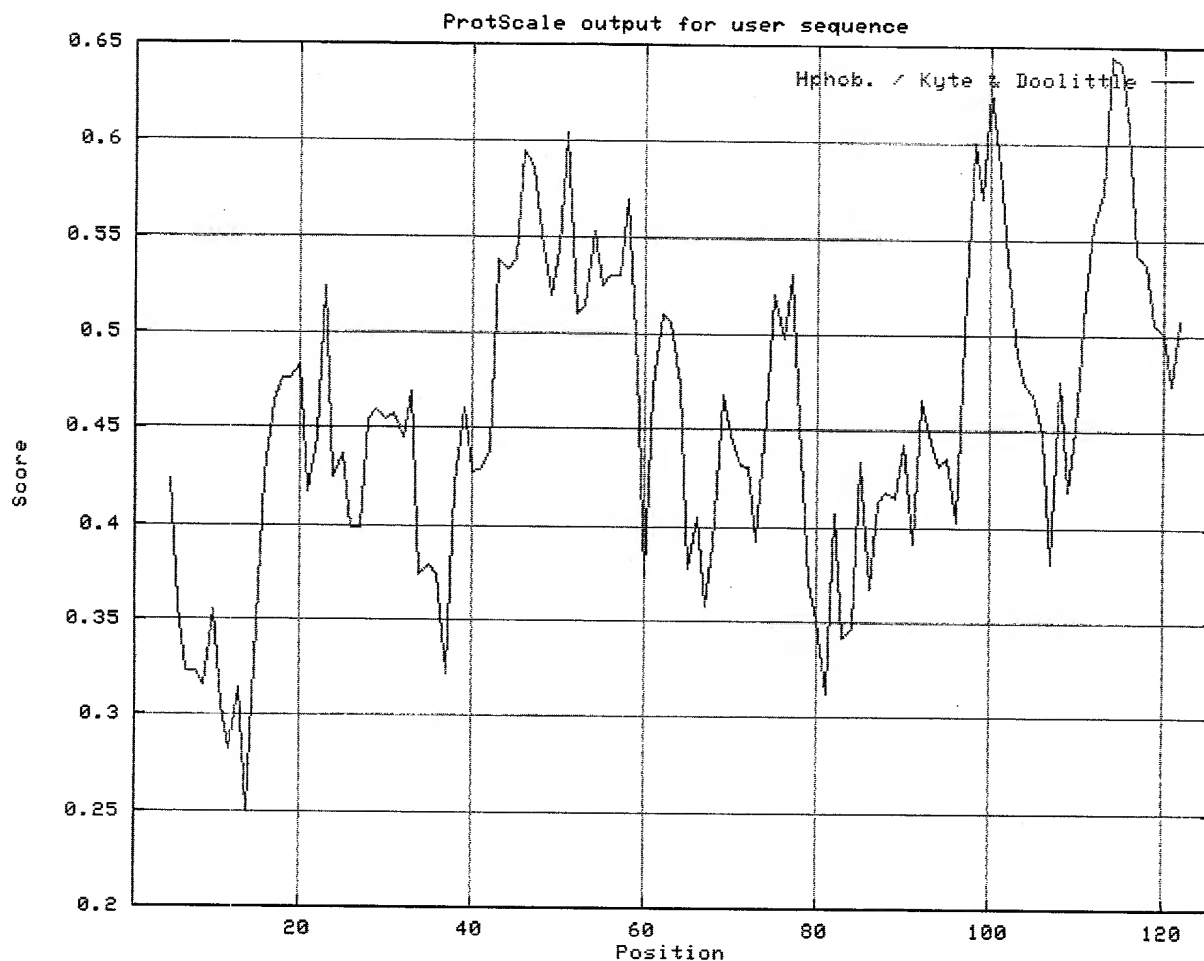


Figure 7A  
121P1F1 % Accessible Residues Profile  
(Janin J., 1979. Nature 277:491-492)

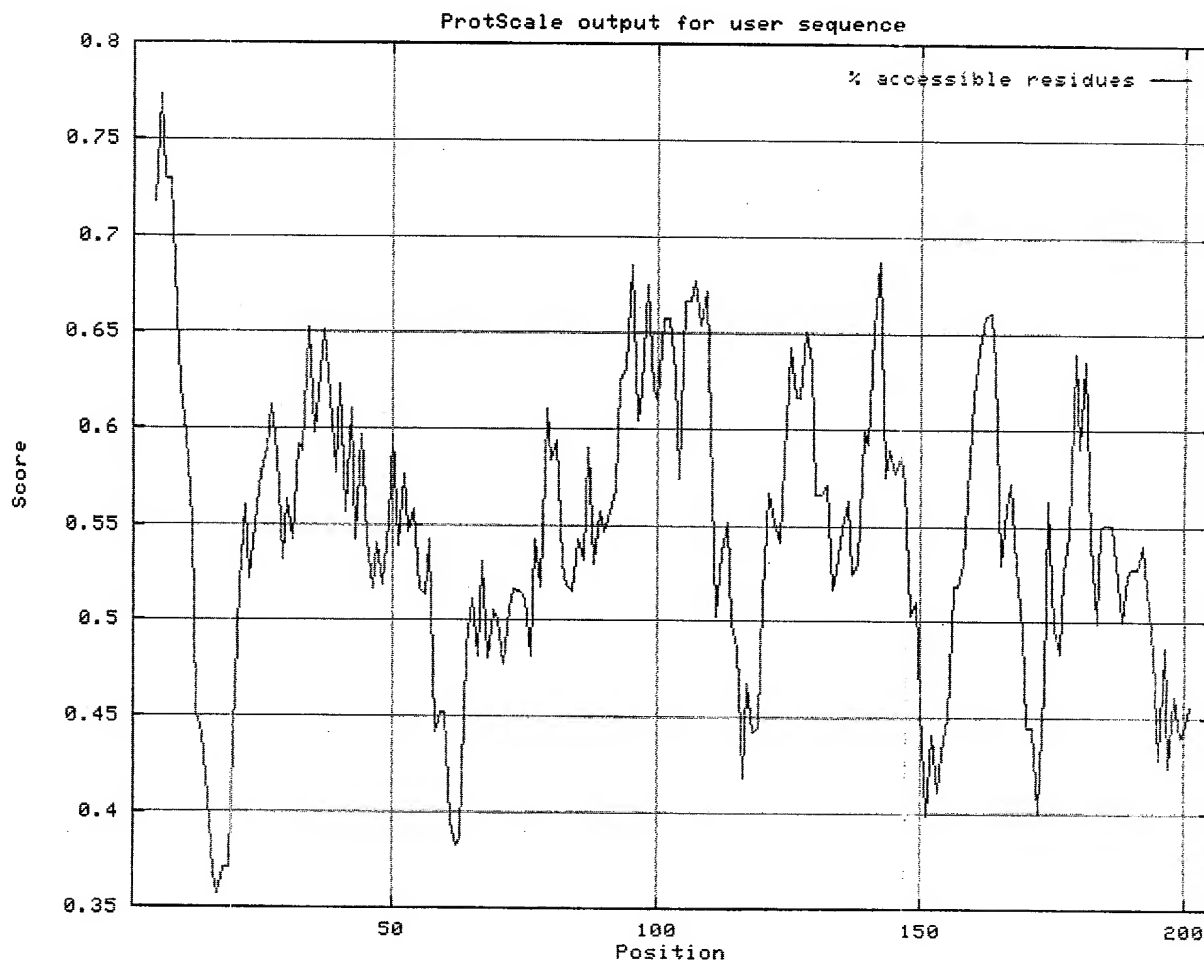


Figure 7B  
121P1F1 variant 1a % Accessible Residues Profile  
(Janin J., 1979. Nature 277:491-492)

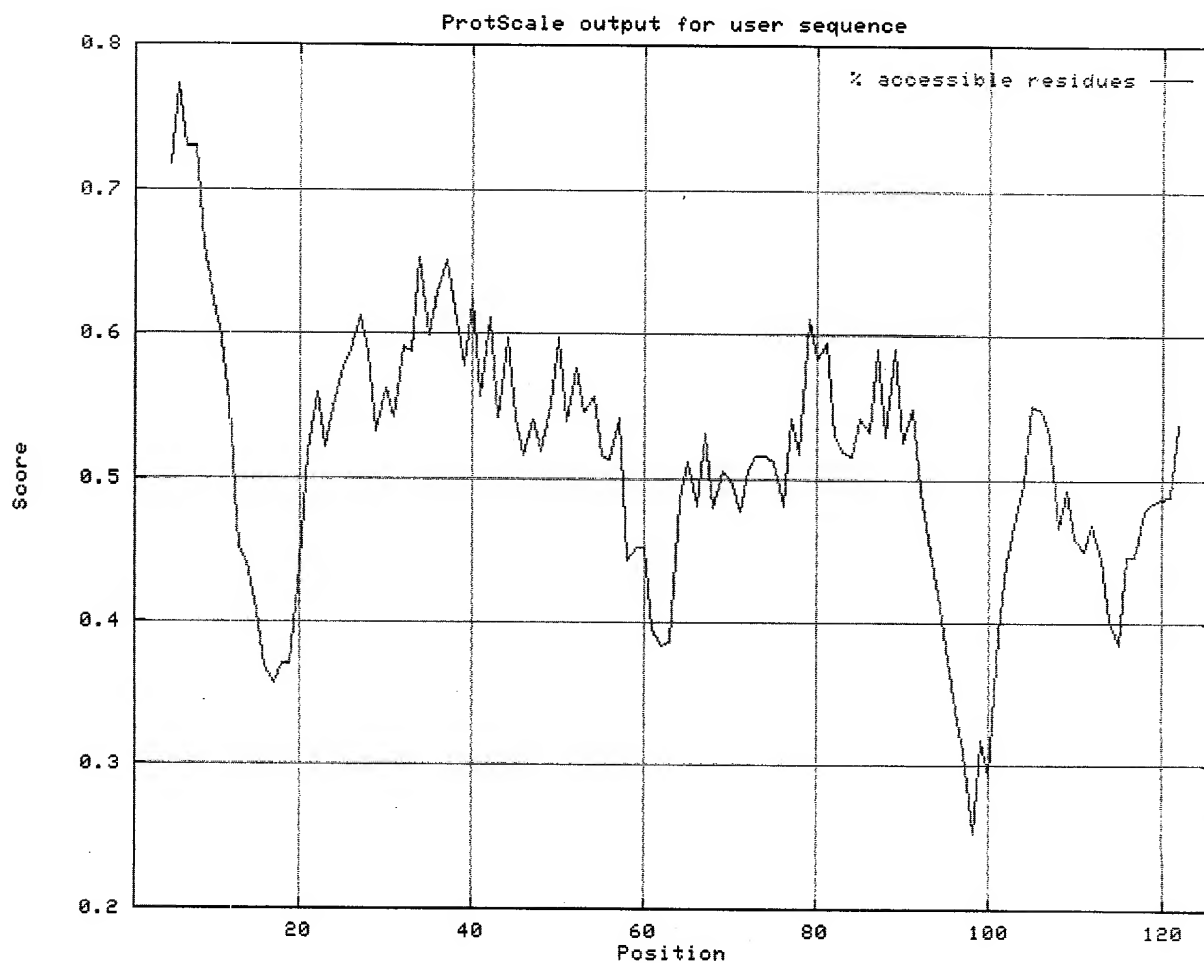


Figure 8A  
121P1F1 Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)

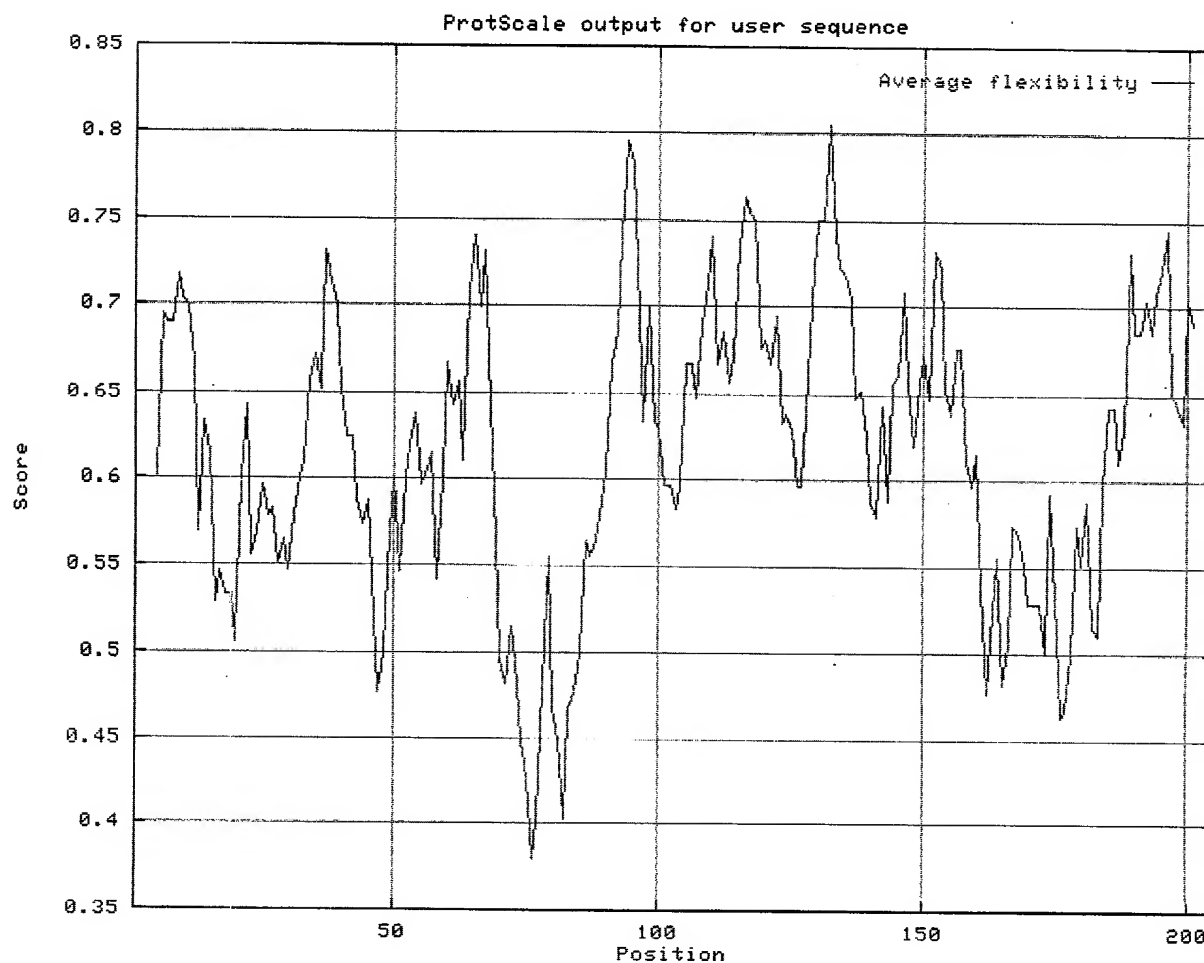


Figure 8B  
121P1F1 variant 1a Average Flexibility Profile  
(Bhaskaran R., Ponnuswamy P.K., 1988.  
Int. J. Pept. Protein Res. 32:242-255)

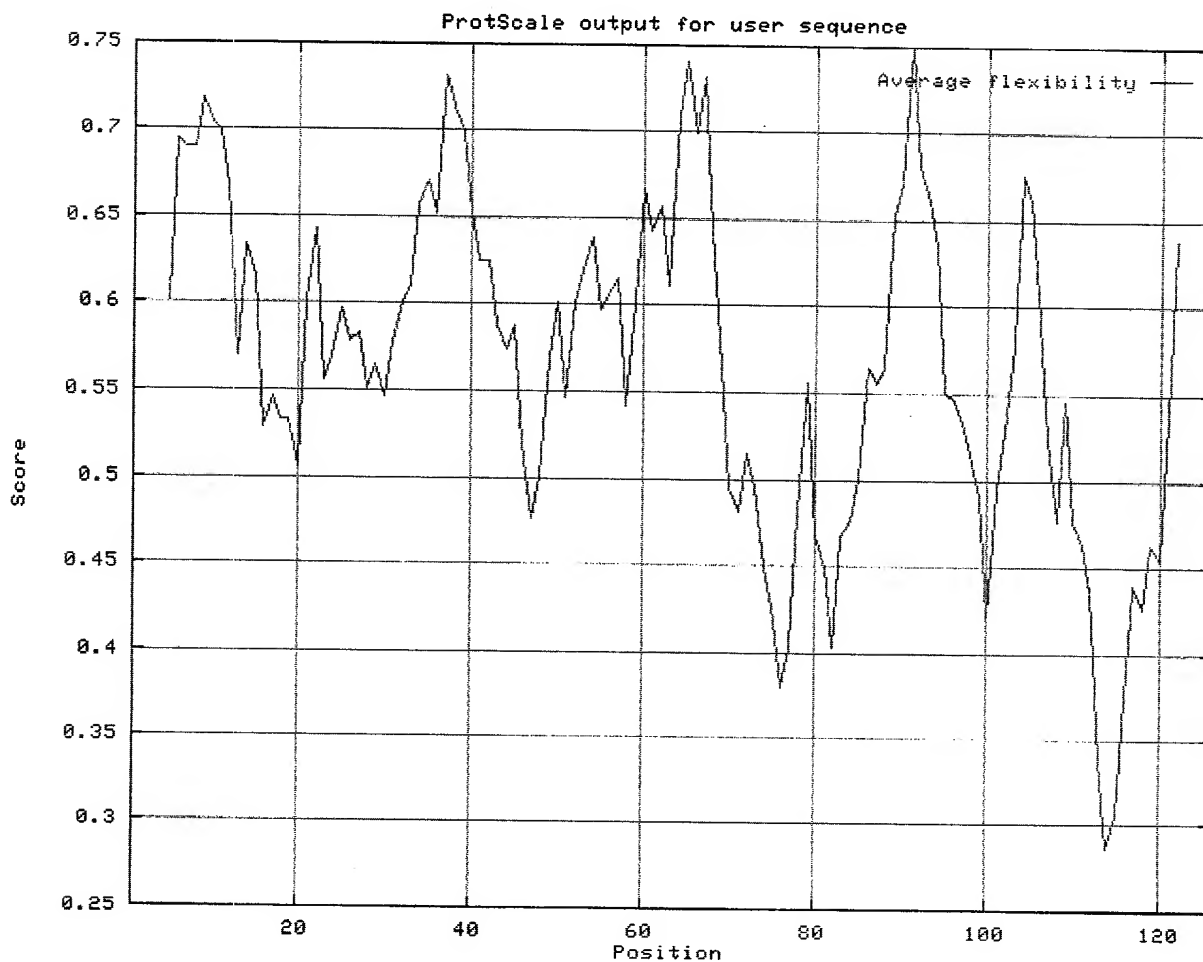


Figure 9A  
121P1F1 Beta-turn Profile  
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

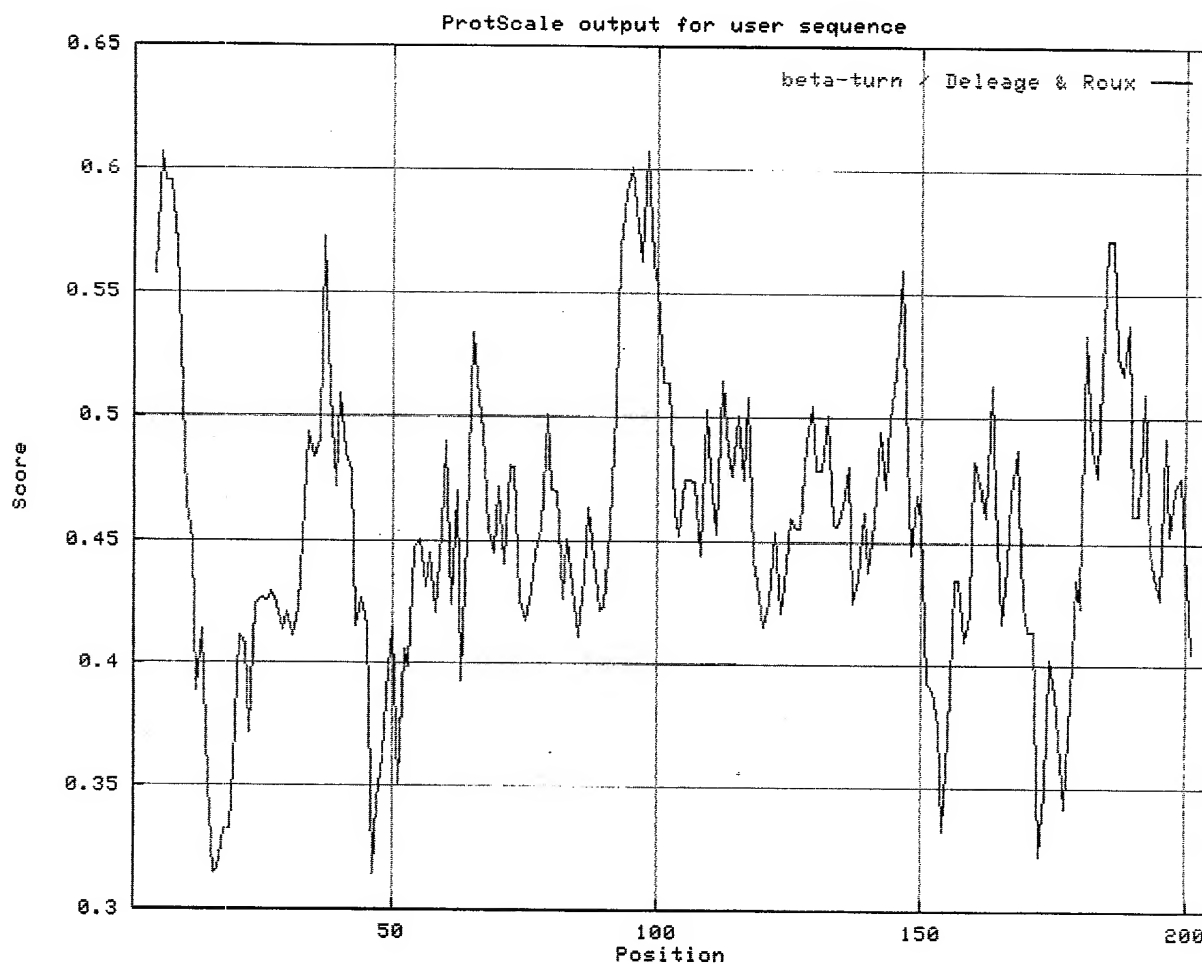
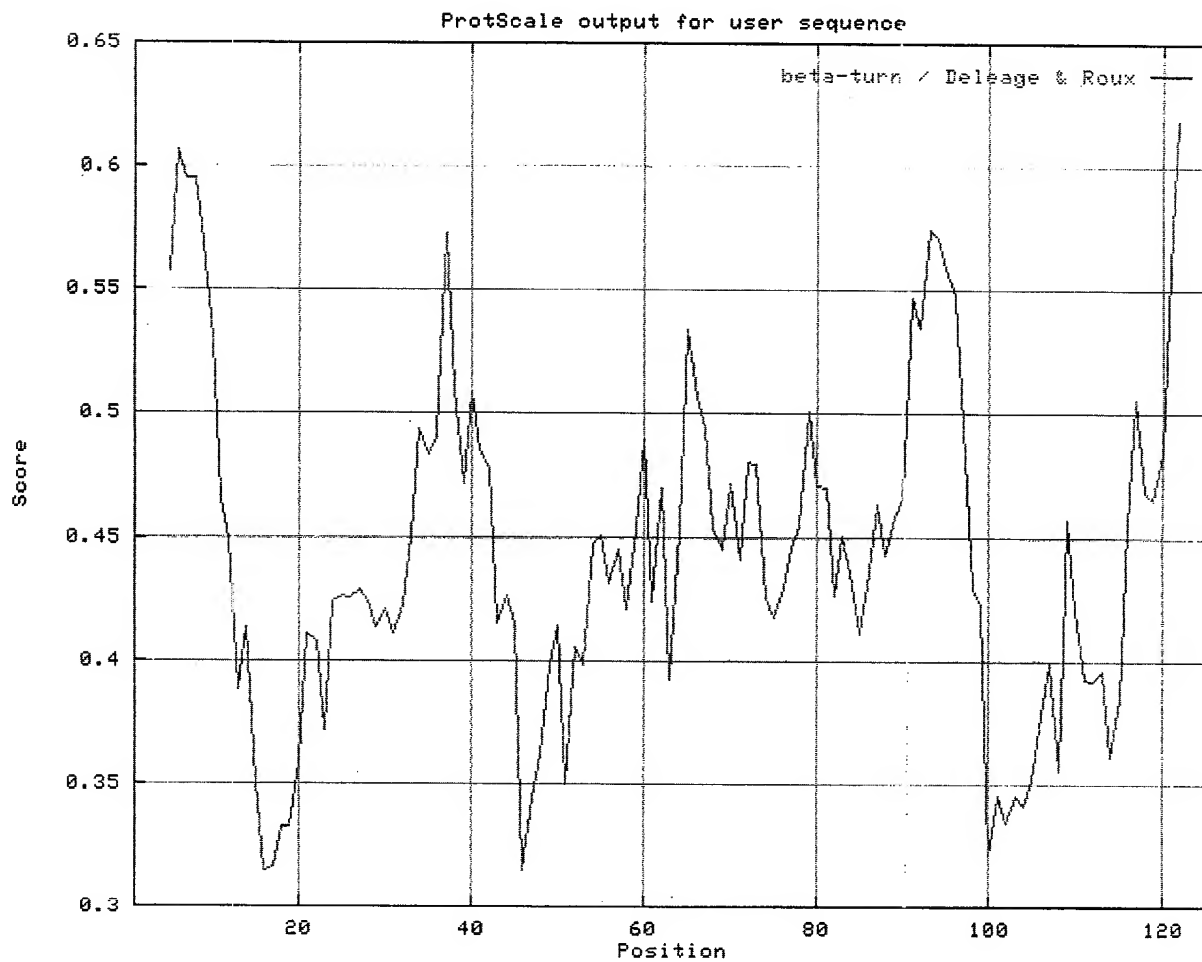
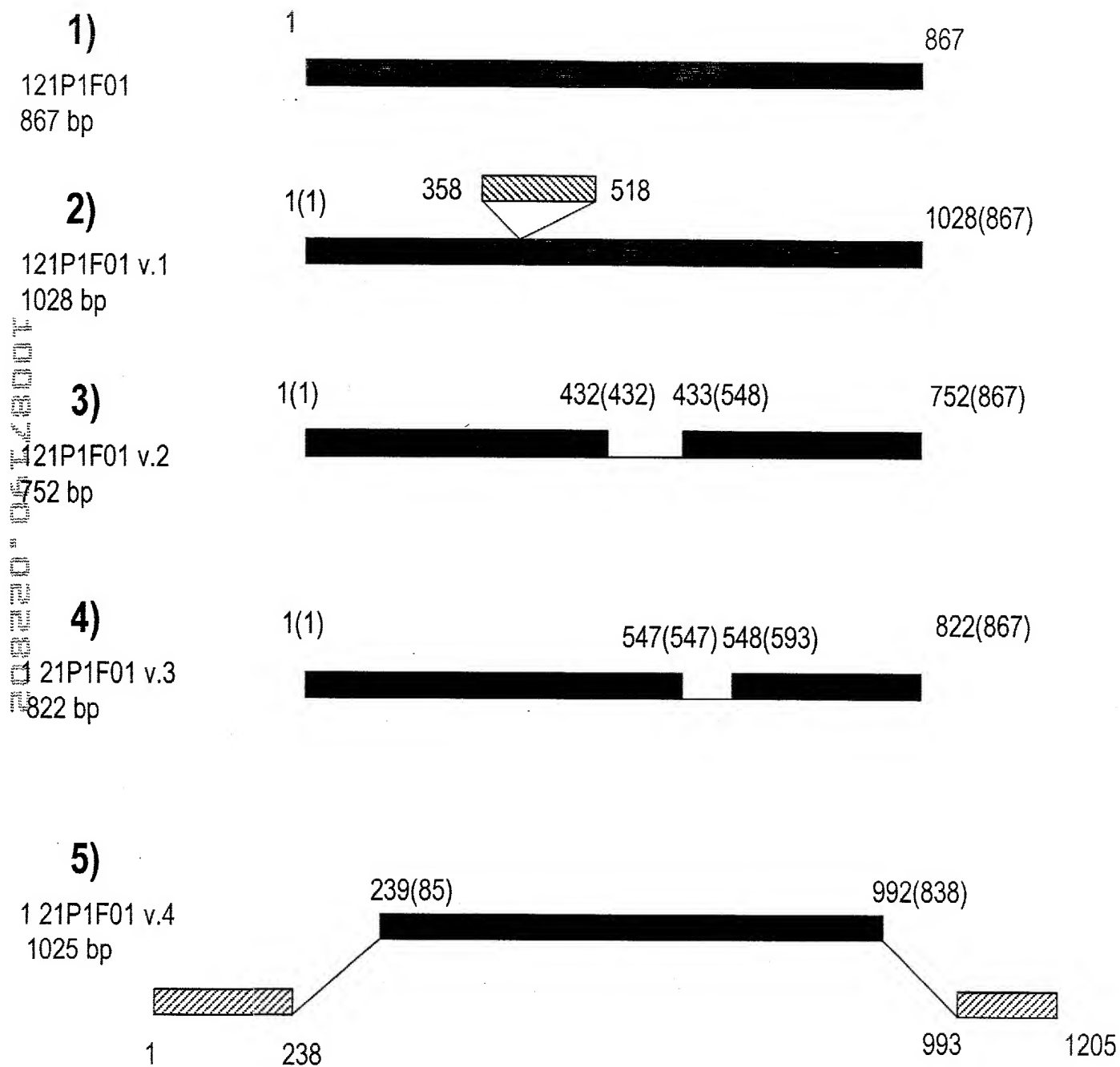


Figure 9B  
121P1F1 variant 1a Beta-turn Profile  
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)

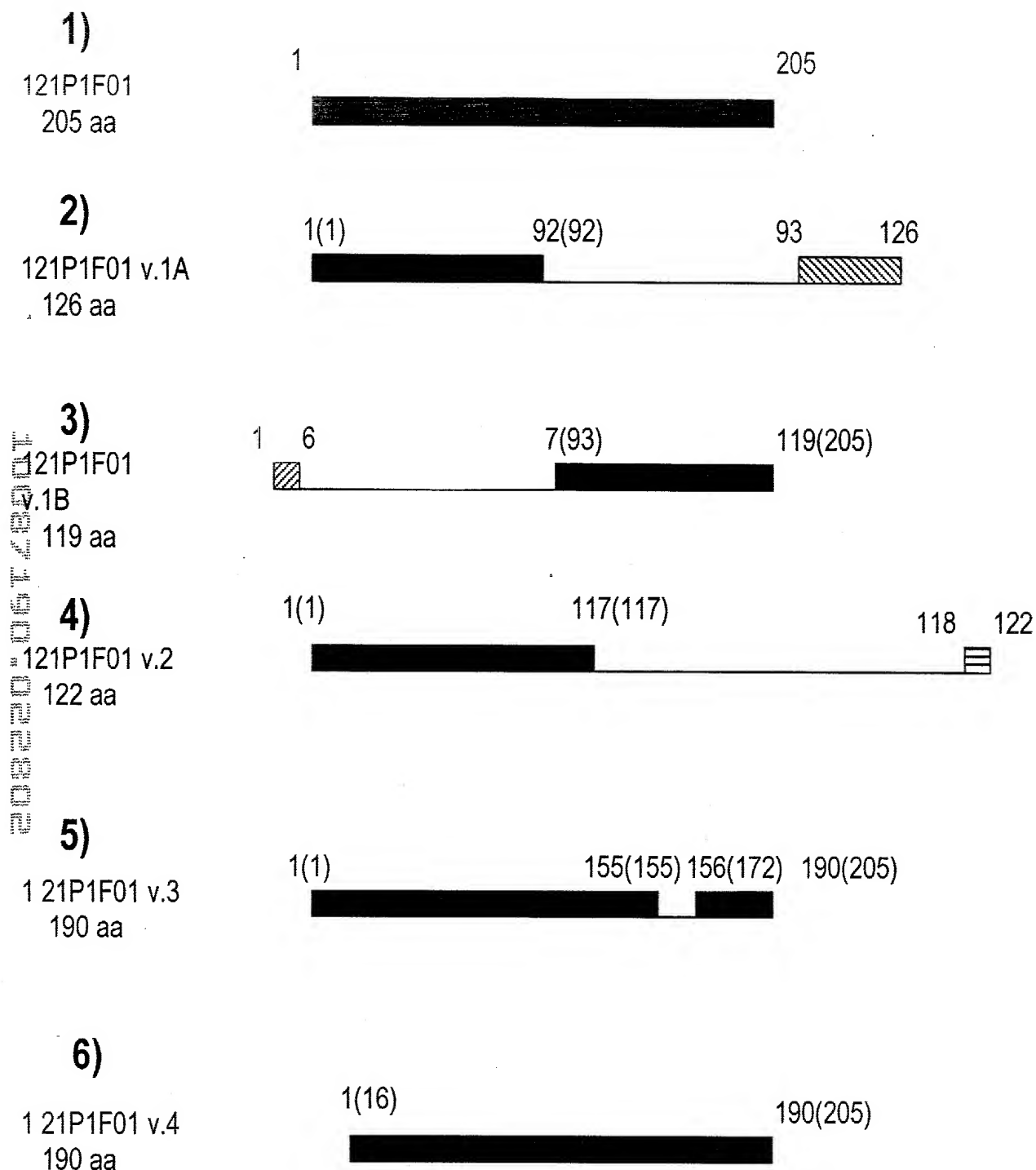


**Figure 10**



Note: Numbers in “()” correspond to those of the original sequence. Black box shows the same sequence as the original one. SNPs are indicated above the box.

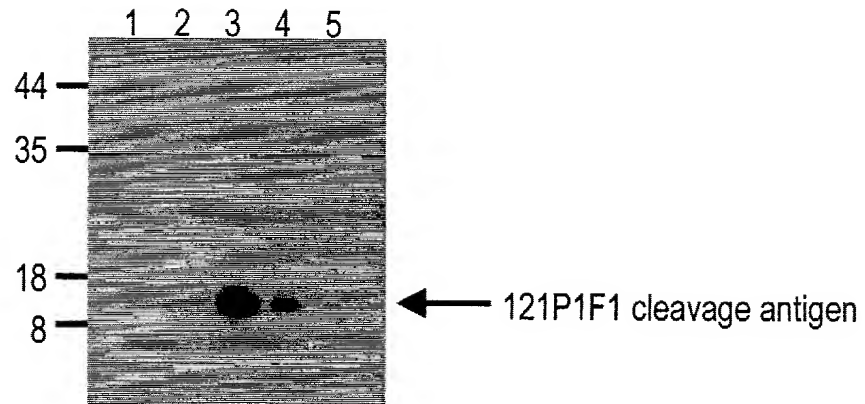
# Figure 11



Note: Numbers in “()” correspond to those of the original sequence. Black box shows the same sequence as the original one. Single amino acid variations are indicated above the box.

**Figure 12**

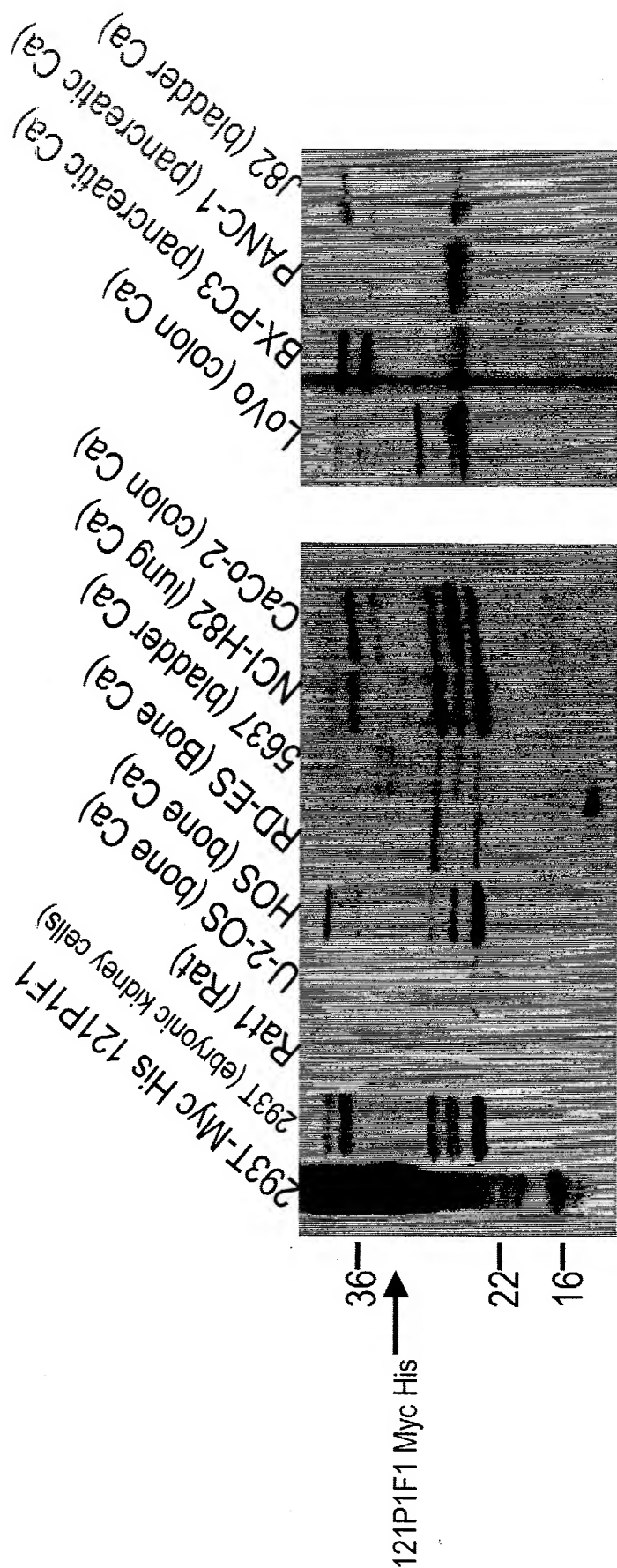
**Specific recognition of 121P1F1 antigen by anti-121P1F1 pAb**



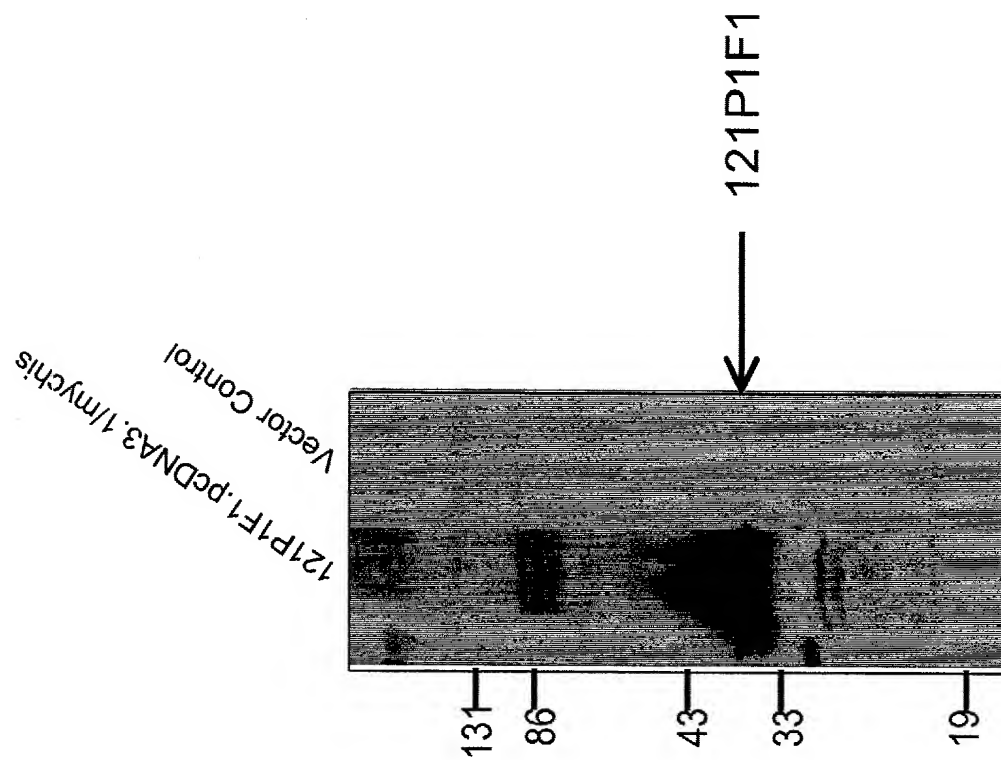
- |                       |         |
|-----------------------|---------|
| 1. Pre-immune         | 1:100   |
| 2. Pre-immune         | 1:1,600 |
| 3. Anti-121P1F1 serum | 1:100   |
| 4. Anti-121P1F1 serum | 1:400   |
| 5. Anti-121P1F1 serum | 1:1,600 |

Figure 13

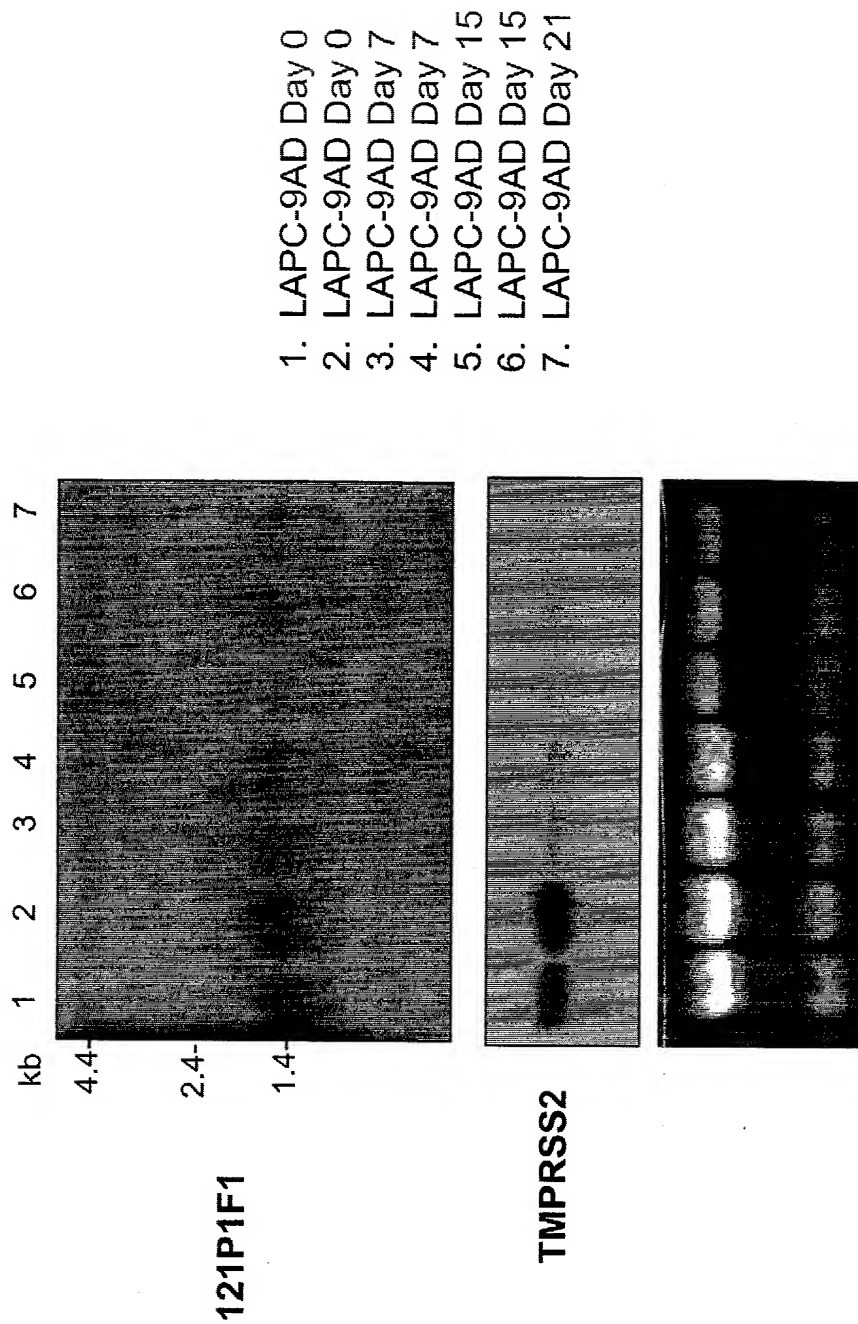
Expression of 121P1F1 in various cancer cells



**Figure 14** Expression of epitope tagged 121P1F1 in 293T cells



**Figure 15** 121P1F1 Androgen Regulation *In Vivo*

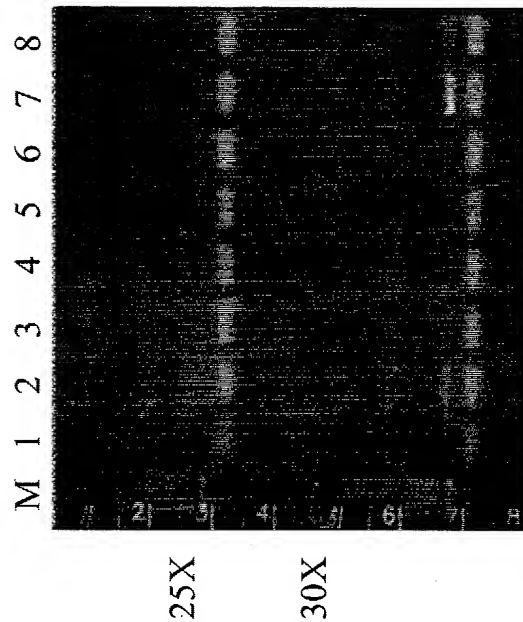






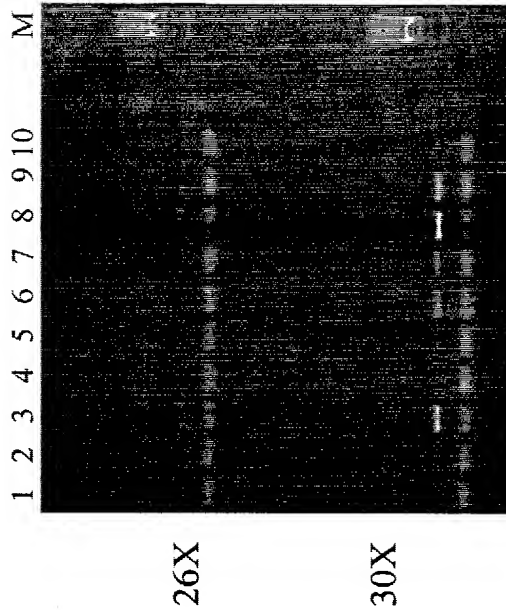
**Figure 17** Expression of 121P1F1 by RT-PCR

**A. Human normal tissues**



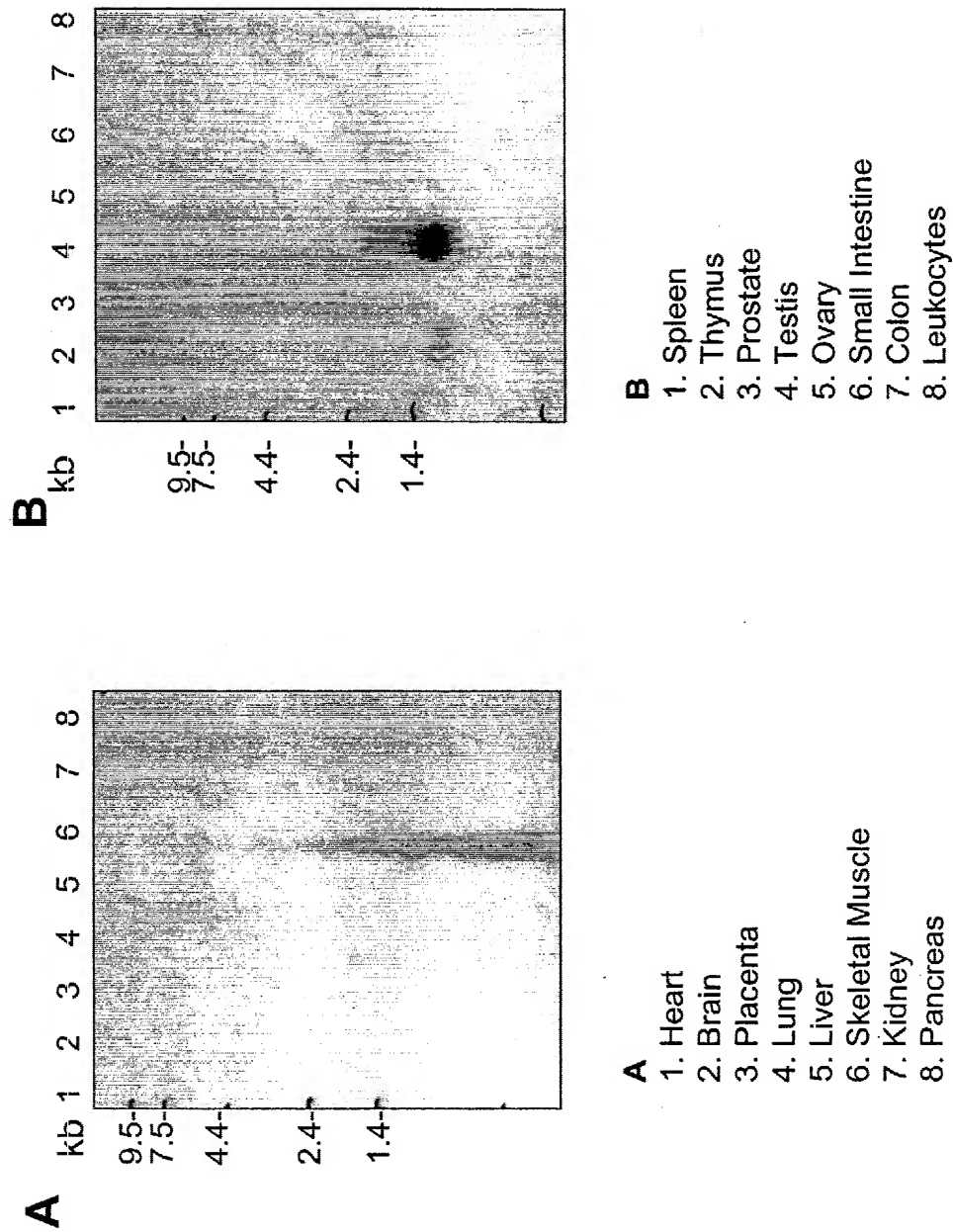
- 1) Colon
- 2) Ovary
- 3) Leuk.
- 4) Prost.
- 5) Small Int.
- 6) Spleen
- 7) Testis
- 8) Thymus

**B. Patient tumor specimens**

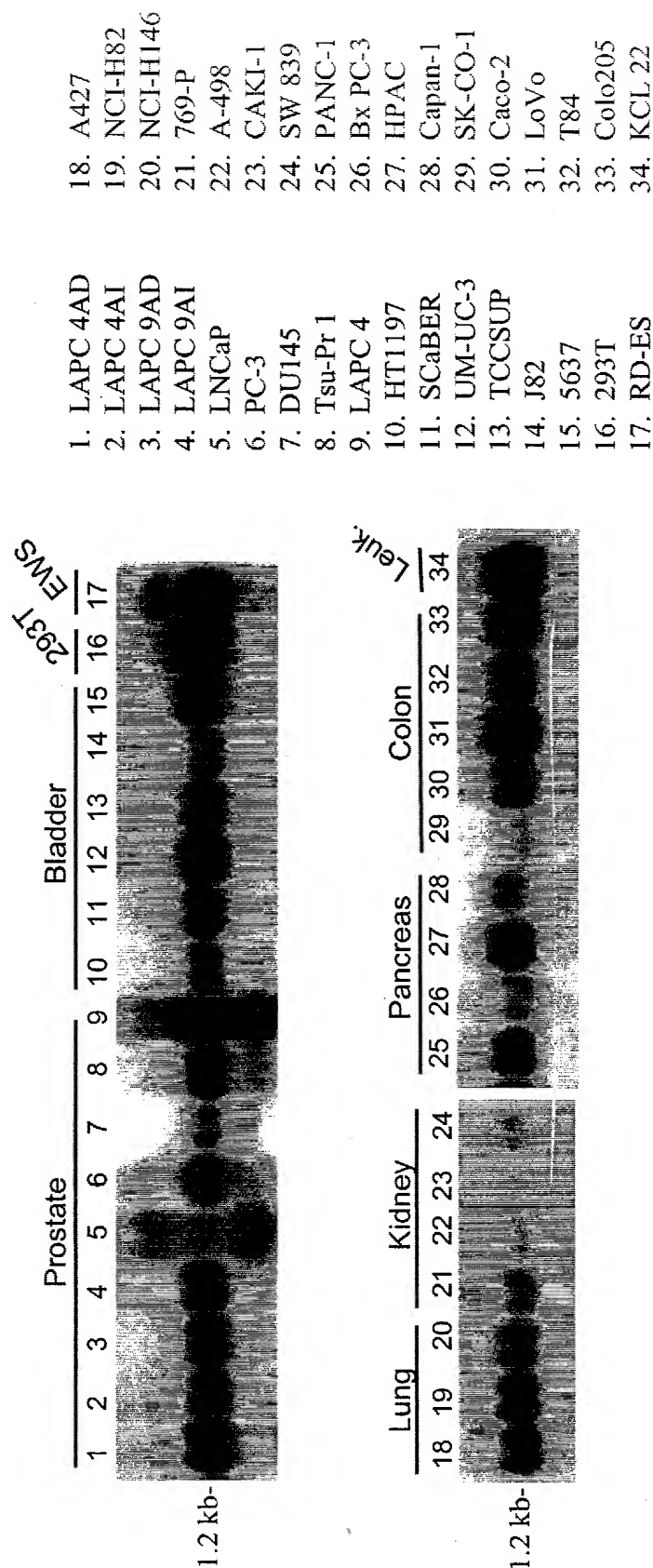


- 1) VP1
- 2) VP2
- 3) XP
- 4) Normal prostate
- 5) Prostate cancer pool
- 6) Bladder cancer pool
- 7) Kidney cancer pool
- 8) Colon cancer pool
- 9) Lung tumor
- 10) H2O

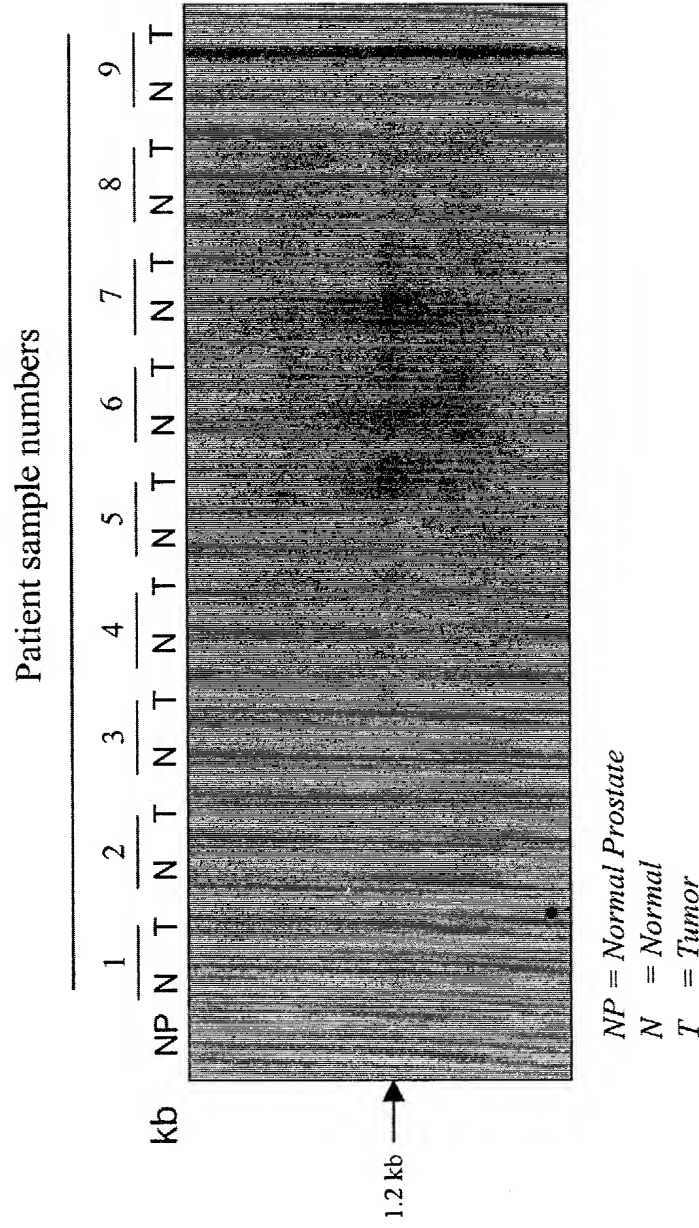
**Figure 18** Expression of 121P1F1 in normal human tissues



**Figure 19** Expression of 121P1F1 in Multiple Cancer Cell lines



**Figure 20** Expression of 121P1F1 in Patient Prostate Cancer Samples



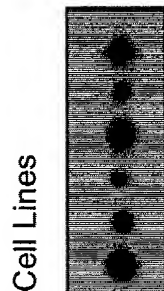
**Figure 21 Expression of 121P1F1 in Kidney, Breast, Cervical and Stomach Patients Samples as well as Cancer Cell lines**



T = tumor RNA  
N = normal adjacent tissue RNA

**Cancer cell lines are:**  
(from left to right)

- HeLa (cervical carcinoma)
- Daudi (Burkitt's lymphoma)
- K562 (CML)
- HL-60 (PML)
- G361 (melanoma)
- A549 (lung carcinoma)
- MOLT-4 (lymphoblastic leuk.)
- SW480 (colorectal carcinoma)
- Raji (Burkitt's lymphoma)



### **Figure 22 Androgen Regulation of 121P1F1**

- LAPC-4<sup>2</sup> FBS
- LAPC-4<sup>2</sup> charcoal-stripped FBS, 14 hrs
- LAPC-4<sup>2</sup> charcoal-stripped FBS, 14 hrs + mib
- LAPC-4<sup>2</sup> charcoal-stripped FBS, 24 hrs
- LAPC-4<sup>2</sup> charcoal-stripped FBS, 24 hrs + mib

